

SYN-128.ST25.txt
SEQUENCE LISTING

<110> Zeneca Limited

<120> Insecticidal Proteins from Paecilomyces and Synergistic Combinations Thereof

<130> SYN-128

<140> US 10/019,823
<141> 2001-12-21

<150> PCT/GB00/02457
<151> 2000-06-23

<150> GB 9915215.9
<151> 1999-06-29

<150> GB 9930536.9
<151> 1999-12-23

<160> 65

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 33
<212> PRT
<213> Paecilomyces sp.

<220>
<221> VARIANT
<222> 1, 2
<223> Xaa = Any Amino Acid

<400> 1
Xaa Xaa Ile Cys Thr Pro Ala Gly Val Lys Cys Pro Ala Ala Leu Pro
1 5 10 15
Cys Cys Pro Gly Leu Arg Cys Ile Gly Gly Val Asn Asn Lys Val Cys
20 25 30
Arg

<210> 2
<211> 33
<212> PRT
<213> Paecilomyces sp.

<400> 2
Gly Lys Ile Cys Thr Pro Ala Gly Val Lys Cys Pro Ala Ala Leu Pro
1 5 10 15
Cys Cys Pro Gly Leu Arg Cys Ile Gly Gly Val Asn Asn Lys Val Cys
20 25 30
Arg

<210> 3
<211> 35
<212> PRT
<213> Paecilomyces sp.

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<220>
<221> VARIANT
<222> 1, 2
<223> Xaa = Any Amino Acid

<400> 3
Xaa Xaa Gly Lys Ile Cys Thr Pro Ala Gly Val Lys Cys Pro Ala Ala
1 5 10 15
Leu Pro Cys Cys Pro Gly Leu Arg Cys Ile Gly Gly Val Asn Asn Lys
20 25 30
Val Cys Arg
35

<210> 4
<211> 332
<212> DNA
<213> Paecilomyces sp.

<400> 4
ggcaagatct gcactcctgc tggagttgt a cgtat tttca tccat ttcct ycaccactcc 60
tctaa catga agcaacttc tcttctctc t ctttgc tcc agaaatgtcc cgcggctt ctttgc tcc 120
ccggacttcg ctgcatcggc ggcgtcaacg taagtccca tggatctggc aagcgagacc 180
ataacatgc gcagataact aaccctggcc gttatagaac aagggtgtga gtcgacatgt 240
tktacaacct ctacaaacgc ggcactaat gacaacggta gtggcggtaa ttctatgttc 300
gcaactttt agcgtggat aagtatgtt c 332

<210> 5
<211> 320
<212> DNA
<213> Paecilomyces sp.

<400> 5
ggggaaattt gtacgcccgc ggggggttgt a cgtat ttc tca tccat ttcct ccaccactcc 60
tctaa catga agcaacttc tcttctctc t ctttgc tcc agaaatgtcc cgcggctt ctttgc tcc 120
ccggacttcg ctgcatcggc ggcgtcaacg taagtccca tcc tgcacacg acgtgaaggc 180
aatgtactga ccctggccgt tatagaacaa ggttgcgtt cgacatgttt tacaacctt 240
acaaacgcgc gcactaatga caacggtagt gccggtaatt ctatgtcgc aactttttag 300
cgtggataa gtatgttc 320

<210> 6
<211> 320
<212> DNA
<213> Paecilomyces sp.

<400> 6
ggggaaatct gtacgcccgc ggggggttgt a cgtat tttca tccat ttcct ccaccactcc 60
tctaa catga agcaacttc tcttctctc t ctttgc tcc araaatgtcc cgcggctt ctttgc tcc 120
ccggacttcg ctgcatcggc ggcgtcaacg taagtccca tcc tgcacacg acgtgaaggc 180
aatgtactga ccctggccgt tatagaacaa ggttgcgtt cgacatgttt tacaacctt 240
acaaacgcgc gcactaatga caacggtagt gccggtaatt ctatgtcgc aactttttag 300
cgtggataa gtatgttc 320

<210> 7
<211> 174
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide codon optimised

<400> 7
atgggtggca gccccggc tgctctgctg ctggccctgg tggccgtgag cctggccgtg 60
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ttaatttata acttttctaa tatatgacca aaacatggtg atgttttagaa atgtcccg 300
gctctccctt gctgccccgg acttcgctgc atcggcggcg tcaacaacaa ggtttgccgg 360
taa 363

<210> 12
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence containing intron and codon
optimised

<400> 12
atgggtggca gcggcagggc tgctctgctg ctggccctgg tggccgttag cctggccgtg 60
gagatccagg cccggcaagat ctgcaccccg gccggcgtgg tttgtttctg cttctacctt 120
tgatataatat ataataatta tcattaatta gtagtaatata aatatttcaa atattttttt 180
caaaataaaa gaatgttagta tatagcaatt gctttctgt agtttataag tgtgtatatt 240
ttaatttata acttttctaa tatatgacca aaacatggtg atgttttagaa gtgccccggc 300
gccctcccggt gctgccccggg cctccgctgc atcggcggcg tgaacaacaa ggtgtgccgc 360
tga 363

<210> 13
<211> 439
<212> DNA
<213> Paecilomyces sp.

<400> 13
tctacttctt catctcacgc catatatcct cccaaaatca cacctttcc ttcaccatgc 60
aaatctccgc cgtcattgtc gcactcttcg ccagcggcgc catggccggc aagatctgca 120
ctccctgtgg agttgtacgt attttcatcc atttcttctyca ccactctct aacatgaagc 180
aactttctct tctctctaga aatgtcccgcc ggctcttctt tgctgccccgg gacttcgtg 240
catcggcggc gtcacacgtaa gtcacccatgg atctggcaag cgagaccata acatgacgca 300
gtataactaac cctggccgtt atagaacaag gttgtgagtc gacatgtkt acaacctcta 360
caaacgcgcg cactaatgac aacggtagtg ccggtaattc tagtgtcgca acttttgagc 420
tggggataag tatgtttcg 439

<210> 14
<211> 102
<212> DNA
<213> Paecilomyces sp.

<400> 14
ggcaagatct gcactcctgc tggagttaaa tgtcccgccg ctcttcctt ctgccccgg 60
cttcgctgca tcggcggcgta caacaacaag gtttggcggt aa 102

<210> 15
<211> 84
<212> DNA
<213> Dahlia sp.

<400> 15
atggtaata gatctgttgc tttttctgct tttgttctta ttctttttgt tttggctatt 60
tcagatatttgc ttctcttttca agga 84

<210> 16
<211> 87
<212> DNA
<213> Artificial Sequence

<220>
<223> Radish signal sequence

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<400> 16
atggctaagt ttgcttctat tattgctctt ttgttgctg cacttgggg ttttgctgca 60
tttgaagctc caactatggt tgaagct 87

<210> 17
<211> 72
<212> DNA
<213> Zea mays

<400> 17
atgggtggca gcggcagggc tgctctgctg ctggccctgg tgccgtgag cctggccgtg 60
gagatccagg cc 72

<210> 18
<211> 90
<212> DNA
<213> Nicotiana sp.

<400> 18
atgggattt ttctttttc acaattgcct tcatttcttc ttgtctctac acttctctta 60
ttcctagtaa tatcccaactc ttgccgtgcc 90

<210> 19
<211> 51
<212> DNA
<213> Paecilomyces sp.

<400> 19
atgcaaatct ccgcgtcat tgtcgcactc ttgcgcagcg ccgcattggc c 51

<210> 20
<211> 28
<212> PRT
<213> Dahlia sp.

<400> 20
Met Val Asn Arg Ser Val Ala Phe Ser Ala Phe Val Leu Ile Leu Phe
1 5 10 15
Val Leu Ala Ile Ser Asp Ile Ala Ser Val Ser Gly
20 25

<210> 21
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> Radish protein target sequence

<400> 21
Met Ala Lys Phe Ala Ser Ile Ile Ala Leu Leu Phe Ala Ala Leu Val
1 5 10 15
Leu Phe Ala Ala Phe Glu Ala Pro Thr Met Val Glu Ala
20 25

<210> 22
<211> 24
<212> PRT
<213> Zea Mays

<400> 22

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Met Gly Gly Ser Gly Arg Ala Ala Leu Leu Leu Ala Leu Val Ala Val
1 5 10 15
Ser Leu Ala Val Glu Ile Gln Ala
20

<210> 23
<211> 30
<212> PRT
<213> Nicotiana sp.

<400> 23
Met Gly Phe Val Leu Phe Ser Gln Leu Pro Ser Phe Leu Leu Val Ser
1 5 10 15
Thr Leu Leu Leu Phe Leu Val Ile Ser His Ser Cys Arg Ala
20 25 30

<210> 24
<211> 17
<212> PRT
<213> Paecilomyces sp.

<400> 24
Met Gln Ile Ser Ala Val Ile Val Ala Leu Phe Ala Ser Ala Ala Met
1 5 10 15
Ala

<210> 25
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Primers

<400> 25
tcgggctcgc atgaattcgc ggccgcattt tttttttttt tttt 44

<210> 26
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Primers

<400> 26
tcgggctcgc atgaattcgc 19

<210> 27
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Primers

<400> 27
atgaattcgc ggccgcat 18

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<210> 28
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primers

<400> 28
tcgggctcgc atgaattcgc g 21

<210> 29
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primers

<400> 29
ctcgcatgaa ttcgcggccg c 21

<210> 30
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Primers

<221> misc_feature
<222> 9, 12, 15
<223> n = A,T,C or G

<400> 30
athtgyacnc cngcngg 17

<210> 31
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primers

<221> misc_feature
<222> 9, 12, 15, 18
<223> n = A,T,C or G

<400> 31
athtgyacnc cngcnggngt 20

<210> 32
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Primers

<221> misc_feature
<222> 3, 6, 9, 12, 15
<223> n = A,T,C or G

<400> 32 acnccngcng gngtnaa	17
<210> 33 <211> 17 <212> DNA <213> Artificial Sequence	
<220> <223> Primers	
<221> misc_feature <222> 3, 12, 15 <223> n = A,T,C or G	
<400> 33 ccntgytgyc cnggnyt	17
<210> 34 <211> 16 <212> DNA <213> Artificial Sequence	
<220> <223> Primers	
<221> misc_feature <222> 2, 14 <223> n = A,T,C or G	
<400> 34 tnaartgyat hggngg	16
<210> 35 <211> 20 <212> DNA <213> Artificial Sequence	
<220> <223> Primers	
<221> misc_feature <222> 3, 6, 18 <223> n = A,T,C or G	
<400> 35 ggngtnaaya ayaargtntg	20
<210> 36 <211> 26 <212> DNA <213> Artificial Sequence	
<220> <223> Primers	
<221> misc_feature <222> 12, 15, 18, 21, 24 <223> n = inosine	
<400> 36 aarathgya cnccngcngg ngtnaa	26

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<210> 37
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Primers

<221> misc_feature
<222> 3, 6, 9, 12, 21, 24
<223> n = inosine

<400> 37
ccngcnggng tnaartgycc ncngc

26

<210> 38
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Primers

<221> misc_feature
<222> 6, 9, 12, 15, 18
<223> n = inosine

<400> 38
tgyccngcng cnytnccntg ytgycc

26

<210> 39
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Primers

<221> misc_feature
<222> 9, 12, 15
<223> n = inosine

<400> 39
tgyathggng gngtnaayaa yaargt

26

<210> 40
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primers

<400> 40
taaatgtccc gcggctcttc c

21

<210> 41
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Primers

<400> 41
cggctttcc ttgctgcccc g

21

<210> 42
<211> 21
<212> DNA
<213> Artificial Sequence<220>
<223> Primers<400> 42
tgctgccccg gacttcgctg c

21

<210> 43
<211> 27
<212> DNA
<213> Artificial Sequence<220>
<223> Primers<221> misc_feature
<222> 23, 24, 25, 26, 27
<223> n = A,T,C or G<400> 43
ggtttaatta cccaaagttt agnnnnnn

27

<210> 44
<211> 22
<212> DNA
<213> Artificial Sequence<220>
<223> Primers<400> 44
ctcaaacttg ggtaattaaa cc

22

<210> 45
<211> 18
<212> DNA
<213> Artificial Sequence<220>
<223> Primers<400> 45
ggtttaatta cccaaagt

18

<210> 46
<211> 18
<212> DNA
<213> Artificial Sequence<220>
<223> Primers<400> 46
taattaccca agtttgag

18

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<210> 47
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primers

<400> 47
ggtttaatta cccaagttt ag 22

<210> 48
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primers

<221> misc_feature
<222> 3, 15, 18, 21
<223> n = inosine

<400> 48
canacyttrt trtnacncc ncc 23

<210> 49
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primers

<400> 49
atgcagcgaa gtccggggca g 21

<210> 50
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primers

<400> 50
ggggcagcaa ggaagagccg c 21

<210> 51
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primers

<400> 51
aagagccgcg ggacattaa c 21

<210> 52
<211> 49
<212> DNA

<213> Artificial Sequence

<220>

<223> Primers

<400> 52

agttaaatgt cccgcggctc ttcccttgcgt cccggactt cgctgcac

49

<210> 53

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Primers

<400> 53

gatgcagcga agtccggg

18

<210> 54

<211> 718

<212> PRT

<213> Artificial Sequence

<220>

<223> PROTEIN crylial Embl. Accession No. X62821

<221> VARIANT

<222> 602

<223> Xaa = Any Amino Acid

<400> 54

Met Lys Leu Lys Asn Gln Asp Lys His Gln Ser Phe Ser Ser Asn Ala
 1 5 10 15
 Lys Val Asp Lys Ile Ser Thr Asp Ser Leu Lys Asn Glu Thr Asp Ile
 20 25 30
 Glu Leu Gln Asn Ile Asn His Glu Asp Cys Leu Lys Met Ser Glu Tyr
 35 40 45
 Glu Asn Val Glu Pro Phe Val Ser Ala Ser Thr Ile Gln Thr Gly Ile
 50 55 60
 Gly Ile Ala Gly Lys Ile Leu Gly Thr Leu Gly Val Pro Phe Ala Gly
 65 70 75 80
 Gln Val Ala Ser Leu Tyr Ser Phe Ile Leu Gly Glu Leu Trp Pro Lys
 85 90 95
 Gly Lys Asn Gln Trp Glu Ile Phe Met Glu His Val Glu Glu Ile Ile
 100 105 110
 Asn Gln Lys Ile Ser Thr Tyr Ala Arg Asn Lys Ala Leu Thr Asp Leu
 115 120 125
 Lys Gly Leu Gly Asp Ala Leu Ala Val Tyr His Asp Ser Leu Glu Ser
 130 135 140
 Trp Val Gly Asn Arg Asn Asn Thr Arg Ala Arg Ser Val Val Lys Ser
 145 150 155 160
 Gln Tyr Ile Ala Leu Glu Leu Met Phe Val Gln Lys Leu Pro Ser Phe
 165 170 175
 Ala Val Ser Gly Glu Glu Val Pro Leu Leu Pro Ile Tyr Ala Gln Ala
 180 185 190
 Ala Asn Leu His Leu Leu Leu Leu Arg Asp Ala Ser Ile Phe Gly Lys
 195 200 205
 Glu Trp Gly Leu Ser Ser Ser Glu Ile Ser Thr Phe Tyr Asn Arg Gln
 210 215 220
 Val Glu Arg Ala Gly Asp Tyr Ser Tyr His Cys Val Lys Trp Tyr Ser
 225 230 235 240
 Thr Gly Leu Asn Asn Leu Arg Gly Thr Asn Ala Glu Ser Trp Val Arg

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245	250	255
Tyr Asn Gln Phe Arg Arg Asp Met Thr Leu Met Val Leu Asp	Leu Val	
260	265	270
Ala Leu Phe Pro Ser Tyr Asp Thr Gln Met Tyr Pro Ile Lys	Thr Thr	
275	280	285
Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Ala Ile Gly	Thr Val His	
290	295	300
Pro His Pro Ser Phe Thr Ser Thr Thr Trp Tyr Asn Asn Asn	Ala Pro	
305	310	315
Ser Phe Ser Ala Ile Glu Ala Ala Val Val Arg Asn Pro His	Leu Leu	
320	325	330
Asp Phe Leu Glu Gln Val Thr Ile Tyr Ser Leu Leu Ser Arg	Trp Ser	
335	340	345
Asn Thr Gln Tyr Met Asn Met Trp Gly Gly His Lys Leu Glu	Phe Arg	
350	355	360
365	370	375
Thr Ile Gly Gly Thr Leu Asn Ile Ser Thr Gln Gly Ser Thr	Asn Thr	
380	385	390
Ser Ile Asn Pro Val Thr Leu Pro Phe Thr Ser Arg Asp Val	Tyr Arg	
400	405	410
Thr Glu Ser Leu Ala Gly Leu Asn Leu Phe Leu Thr Gln Pro	Val Asn	
415	420	425
Val Pro Arg Val Asp Phe His Trp Lys Phe Val Thr His Pro	Ile Ala	
430	435	440
Ser Asp Asn Phe Tyr Tyr Pro Gly Tyr Ala Gly Ile Gly	Thr Gln Leu	
445	450	455
Gln Asp Ser Glu Asn Glu Leu Pro Pro Glu Ala Thr Gly	Gln Pro Asn	
460	465	470
Tyr Glu Ser Tyr Ser His Arg Leu Ser His Ile Gly Leu Ile	Ser Ala	
480	485	490
Ser His Val Lys Ala Leu Val Tyr Ser Trp Thr His Arg Ser	Ala Asp	
495	500	505
Arg Thr Asn Thr Ile Glu Pro Asn Ser Ile Thr Gln Ile Pro	Leu Val	
510	515	520
Lys Ala Phe Asn Leu Ser Ser Gly Ala Ala Val Val Arg	Gly Pro Gly	
525	530	535
Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Asn Thr Gly	Thr Phe Gly	
540	545	550
Asp Ile Arg Val Asn Ile Asn Pro Pro Phe Ala Gln Arg	Tyr Arg Val	
560	565	570
Arg Ile Arg Tyr Ala Ser Thr Thr Asp Leu Gln Phe His	Thr Ser Ile	
575	580	585
Asn Gly Lys Ala Ile Asn Gln Gly Asn Phe Ser Ala Thr	Met Asn Arg	
590	595	600
Gly Glu Asp Leu Asp Tyr Lys Thr Phe Xaa Thr Val Gly	Phe Thr Thr	
605	610	615
Pro Phe Ser Leu Leu Asp Val Gln Ser Thr Phe Thr Ile	Gly Ala Trp	
620	625	630
Asn Phe Ser Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile	Glu Phe Val	
640	645	650
Pro Val Glu Val Thr Tyr Glu Ala Glu Tyr Asp Phe	Glu Lys Ala Gln	
655	660	665
Glu Lys Val Thr Ala Leu Phe Thr Ser Thr Asn Pro Arg	Gly Leu Lys	
670	675	680
Thr Asp Val Lys Asp Tyr His Ile Asp Gln Val Ser Asn	Leu Val Glu	
685	690	695
Ser Leu Ser Asp Glu Phe Tyr Leu Asp Glu Lys Arg	Glu Leu Phe Glu	
700	705	710
Ile Val Lys Tyr Ala Lys Gln Leu His Ile Glu Arg Asn Met	715	

<210> 55
<211> 719

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<212> PRT

<213> Artificial Sequence

<220>

<223> PROTEIN cry1Ia2 Emb1. Accession No. M98544

<400> 55

Met Lys Leu Lys Asn Gln Asp Lys His Gln Ser Phe Ser Ser Asn Ala
 1 5 10 15
 Lys Val Asp Lys Ile Ser Thr Asp Ser Leu Lys Asn Glu Thr Asp Ile
 20 25 30
 Glu Leu Gln Asn Ile Asn His Glu Asp Cys Leu Lys Met Ser Glu Tyr
 35 40 45
 Glu Asn Val Glu Pro Phe Val Ser Ala Ser Thr Ile Gln Thr Gly Ile
 50 55 60
 Gly Ile Ala Gly Lys Ile Leu Gly Thr Leu Gly Val Pro Phe Ala Gly
 65 70 75 80
 Gln Val Ala Ser Leu Tyr Ser Phe Ile Leu Gly Glu Leu Trp Pro Lys
 85 90 95
 Gly Lys Asn Gln Trp Glu Ile Phe Met Glu His Val Glu Glu Ile Ile
 100 105 110
 Asn Gln Lys Ile Ser Thr Tyr Ala Arg Asn Lys Ala Leu Thr Asp Leu
 115 120 125
 Lys Gly Leu Gly Asp Ala Leu Ala Val Tyr His Asp Ser Leu Glu Ser
 130 135 140
 Trp Val Gly Asn Arg Asn Asn Thr Arg Ala Arg Ser Val Val Lys Ser
 145 150 155 160
 Gln Tyr Ile Ala Leu Glu Leu Met Phe Val Gln Lys Leu Pro Ser Phe
 165 170 175
 Ala Val Ser Gly Glu Glu Val Pro Leu Leu Pro Ile Tyr Ala Gln Ala
 180 185 190
 Ala Asn Leu His Leu Leu Leu Leu Arg Asp Ala Ser Ile Phe Gly Lys
 195 200 205
 Glu Trp Gly Leu Ser Ser Ser Glu Ile Ser Thr Phe Tyr Asn Arg Gln
 210 215 220
 Val Glu Arg Ala Gly Asp Tyr Ser Asp His Cys Val Lys Trp Tyr Ser
 225 230 235 240
 Thr Gly Leu Asn Asn Leu Arg Gly Thr Asn Ala Glu Ser Trp Val Arg
 245 250 255
 Tyr Asn Gln Phe Arg Arg Asp Met Thr Leu Met Val Leu Asp Leu Val
 260 265 270
 Ala Leu Phe Pro Ser Tyr Asp Thr Gln Met Tyr Pro Ile Lys Thr Thr
 275 280 285
 Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Ala Ile Gly Thr Val His
 290 295 300
 Pro His Pro Ser Phe Thr Ser Thr Thr Trp Tyr Asn Asn Asn Ala Pro
 305 310 315 320
 Ser Phe Ser Ala Ile Glu Ala Ala Val Val Arg Asn Pro His Leu Leu
 325 330 335
 Asp Phe Leu Glu Gln Val Thr Ile Tyr Ser Leu Leu Ser Arg Trp Ser
 340 345 350
 Asn Thr Gln Tyr Met Asn Met Trp Gly Gly His Lys Leu Glu Phe Arg
 355 360 365
 Thr Ile Gly Gly Thr Leu Asn Ile Ser Thr Gln Gly Ser Thr Asn Thr
 370 375 380
 Ser Ile Asn Pro Val Thr Leu Pro Phe Thr Ser Arg Asp Val Tyr Arg
 385 390 395 400
 Thr Glu Ser Leu Ala Gly Leu Asn Leu Phe Leu Thr Gln Pro Val Asn
 405 410 415
 Gly Val Pro Arg Val Asp Phe His Trp Lys Phe Val Thr His Pro Ile
 420 425 430
 Ala Ser Asp Asn Phe Tyr Tyr Pro Gly Tyr Ala Gly Ile Gly Thr Gln
 435 440 445

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Leu Gln Asp Ser Glu Asn Glu Leu Pro Pro Glu Ala Thr Gly Gln Pro
 450 455 460
 Asn Tyr Glu Ser Tyr Ser His Arg Leu Ser His Ile Gly Leu Ile Ser
 465 470 475 480
 Ala Ser His Val Lys Ala Leu Val Tyr Ser Trp Thr His Arg Ser Ala
 485 490 495
 Asp Arg Thr Asn Thr Ile Glu Pro Asn Ser Ile Thr Gln Ile Pro Leu
 500 505 510
 Val Lys Ala Phe Asn Leu Ser Ser Gly Ala Ala Val Val Arg Gly Pro
 515 520 525
 Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Asn Thr Gly Thr Phe
 530 535 540
 Gly Asp Ile Arg Val Asn Ile Asn Pro Pro Phe Ala Gln Arg Tyr Arg
 545 550 555 560
 Val Arg Ile Arg Tyr Ala Ser Thr Thr Asp Leu Gln Phe His Thr Ser
 565 570 575
 Ile Asn Gly Lys Ala Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Asn
 580 585 590
 Arg Gly Glu Asp Leu Asp Tyr Lys Thr Phe Arg Thr Val Gly Phe Thr
 595 600 605
 Thr Pro Phe Ser Phe Leu Asp Val Gln Ser Thr Phe Thr Ile Gly Ala
 610 615 620
 Trp Asn Phe Ser Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe
 625 630 635 640
 Val Pro Val Glu Val Thr Tyr Glu Ala Glu Tyr Asp Phe Glu Lys Ala
 645 650 655
 Gln Glu Lys Val Thr Ala Leu Phe Thr Ser Thr Asn Pro Arg Gly Leu
 660 665 670
 Lys Thr Asp Val Lys Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val
 675 680 685
 Glu Ser Leu Ser Asp Glu Phe Tyr Leu Asp Glu Lys Arg Glu Leu Phe
 690 695 700
 Glu Ile Val Lys Tyr Ala Lys Gln Leu His Ile Glu Arg Asn Met
 705 710 715

<210> 56

<211> 719

<212> PRT

<213> Artificial Sequence

<220>

<223> PROTEIN cry1Ia3 EmbL. Accession No. L36338

<400> 56

Met Lys Leu Lys Asn Gln Asp Lys His Gln Ser Phe Ser Ser Asn Ala
 1 5 10 15
 Lys Val Asp Lys Ile Ser Thr Asp Ser Leu Lys Asn Glu Thr Asp Ile
 20 25 30
 Glu Leu Gln Asn Ile Asn His Glu Asp Cys Leu Lys Met Ser Glu Tyr
 35 40 45
 Glu Asn Val Glu Pro Phe Val Ser Ala Ser Thr Ile Gln Thr Gly Ile
 50 55 60
 Gly Ile Ala Gly Lys Ile Leu Gly Thr Leu Gly Val Pro Phe Ala Gly
 65 70 75 80
 Gln Val Ala Ser Leu Tyr Ser Phe Ile Leu Gly Glu Leu Trp Pro Lys
 85 90 95
 Gly Lys Asn Gln Trp Glu Ile Phe Met Glu His Val Glu Glu Ile Ile
 100 105 110
 Asn Gln Lys Ile Ser Thr Tyr Ala Arg Asn Lys Ala Leu Thr Asp Leu
 115 120 125
 Lys Gln Leu Gly Asp Ala Leu Ala Val Tyr His Asp Ser Leu Glu Ser
 130 135 140

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Trp Val Gly Asn Arg Asn Asn Thr Arg Ala Arg Ser Val Val Lys Ser
 145 150 155 160
 Gln Tyr Ile Ala Leu Glu Leu Met Phe Val Gln Lys Leu Pro Ser Phe
 165 170 175
 Ala Val Ser Gly Glu Glu Val Pro Leu Leu Pro Ile Tyr Ala Gln Ala
 180 185 190
 Ala Asn Leu His Leu Leu Leu Arg Asp Ala Ser Ile Phe Gly Lys
 195 200 205
 Glu Trp Gly Leu Ser Ser Glu Ile Ser Thr Phe Tyr Asn Arg Gln
 210 215 220
 Val Glu Arg Ala Gly Asp Tyr Ser Tyr His Cys Val Lys Trp Tyr Ser
 225 230 235 240
 Thr Gly Leu Asn Asn Leu Arg Gly Thr Asn Ala Glu Ser Trp Val Arg
 245 250 255
 Tyr Asn Gln Phe Arg Arg Asp Met Thr Leu Met Val Leu Asp Leu Val
 260 265 270
 Ala Leu Phe Pro Ser Tyr Asp Thr Gln Met Tyr Pro Ile Lys Thr Thr
 275 280 285
 Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Ala Ile Gly Thr Val His
 290 295 300
 Pro His Pro Ser Phe Thr Ser Thr Trp Tyr Asn Asn Asn Ala Pro
 305 310 315 320
 Ser Phe Ser Ala Ile Glu Ala Ala Val Val Arg Asn Pro His Leu Leu
 325 330 335
 Asp Phe Leu Glu Gln Val Thr Ile Tyr Ser Leu Leu Ser Arg Trp Ser
 340 345 350
 Asn Thr Gln Tyr Met Asn Met Trp Gly Gly His Lys Leu Glu Phe Arg
 355 360 365
 Thr Ile Gly Gly Thr Leu Asn Ile Ser Thr Gln Gly Ser Thr Asn Thr
 370 375 380
 Ser Ile Asn Pro Val Thr Leu Pro Phe Thr Ser Arg Asp Val Tyr Arg
 385 390 395 400
 Thr Glu Ser Leu Ala Gly Leu Asn Leu Phe Leu Thr Gln Pro Val Asn
 405 410 415
 Gly Val Pro Arg Val Asp Phe His Trp Lys Phe Val Thr His Pro Ile
 420 425 430
 Ala Ser Asp Asn Phe Tyr Tyr Pro Gly Tyr Ala Gly Ile Gly Thr Gln
 435 440 445
 Leu Gln Asp Ser Glu Asn Glu Leu Pro Pro Glu Ala Thr Gly Gln Pro
 450 455 460
 Asn Tyr Glu Ser Tyr Ser His Arg Leu Ser His Ile Gly Leu Ile Ser
 465 470 475 480
 Ala Ser His Val Lys Ala Leu Val Tyr Ser Trp Thr His Arg Ser Ala
 485 490 495
 Asp Arg Thr Asn Thr Ile Glu Pro Asn Ser Ile Thr Gln Ile Pro Leu
 500 505 510
 Val Lys Ala Phe Asn Leu Ser Ser Gly Ala Ala Val Val Arg Gly Pro
 515 520 525
 Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Asn Thr Gly Thr Phe
 530 535 540
 Gly Asp Ile Arg Val Asn Ile Asn Pro Pro Phe Ala Gln Arg Tyr Arg
 545 550 555 560
 Val Arg Ile Arg Tyr Ala Ser Thr Thr Asp Leu Gln Phe His Thr Ser
 565 570 575
 Ile Asn Gly Lys Ala Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Asn
 580 585 590
 Arg Gly Glu Asp Leu Asp Tyr Lys Thr Phe Arg Thr Val Gly Phe Thr
 595 600 605
 Thr Pro Phe Ser Phe Leu Asp Val Gln Ser Thr Phe Thr Ile Gly Ala
 610 615 620
 Trp Asn Phe Ser Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe
 625 630 635 640
 Val Pro Val Glu Val Thr Tyr Glu Ala Glu Tyr Asp Phe Glu Lys Ala

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Gln	Glu	Lys	Val	645	650	655
660	665	670				
Lys	Thr	Asp	Val	Lys	Asp	Tyr
675	680	685				
Glu	Ser	Leu	Ser	Asp	Glu	Phe
690	695	700				
Glu	Ile	Val	Lys	Tyr	Ala	Asn
705	710	715				

<210> 57
<211> 719
<212> PRT
<213> Artificial Sequence

<220>
<223> PROTEIN cry1Ia4 EmbL. Accession No. L49391

<400> 57						
Met	Lys	Leu	Lys	Asn	Gln	Asp
1	5	10	15			
Lys	Val	Asp	Lys	Ile	Ser	Thr
20	25	30				
Glu	Leu	Gln	Asn	Ile	Asn	His
35	40	45				
Glu	Asn	Val	Glu	Pro	Phe	Val
50	55	60				
Gly	Ile	Ala	Gly	Ile	Leu	Gly
65	70	75	80			
Gln	Val	Ala	Ser	Leu	Tyr	Ser
85	90	95				
Gly	Lys	Asn	Gln	Trp	Glu	Ile
100	105	110				
Asn	Gln	Lys	Ile	Ser	Thr	Tyr
115	120	125				
Lys	Gly	Leu	Gly	Asp	Ala	Leu
130	135	140				
Trp	Val	Gly	Asn	Arg	Asn	Asn
145	150	155				
Gln	Tyr	Ile	Ala	Leu	Glu	Leu
165	170	175				
Ala	Val	Ser	Gly	Glu	Val	Pro
180	185	190				
Ala	Asn	Leu	His	Leu	Leu	Leu
195	200	205				
Glu	Trp	Gly	Leu	Ser	Ser	Glu
210	215	220				
Val	Glu	Arg	Ala	Gly	Asp	Tyr
225	230	235				
Thr	Gly	Leu	Asn	Asn	Leu	Arg
245	250	255				
Tyr	Asn	Gln	Phe	Arg	Arg	Asp
260	265	270				
Ala	Leu	Phe	Pro	Ser	Tyr	Asp
275	280	285				
Ala	Gln	Leu	Thr	Arg	Glu	Val
290	295	300				
Pro	His	Pro	Ser	Phe	Thr	Ser
305	310	315				
Ser	Phe	Ser	Ala	Ile	Glu	Ala
325	330	335				
Asp	Phe	Leu	Glu	Gln	Val	Thr

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Asn	Thr	Gln	Tyr	Met	Asn	Met	Trp	Gly	Gly	His	Lys	Leu	Glu	Phe	Arg
340					345							350			
355					360							365			
Thr	Ile	Gly	Gly	Thr	Leu	Asn	Ile	Ser	Thr	Gln	Gly	Ser	Thr	Asn	Thr
370					375						380				
Ser	Ile	Asn	Pro	Val	Thr	Leu	Pro	Phe	Thr	Ser	Arg	Asp	Val	Tyr	Arg
385					390					395			400		
Thr	Glu	Ser	Leu	Ala	Gly	Leu	Asn	Leu	Phe	Leu	Thr	Gln	Pro	Val	Asn
											410			415	
Gly	Val	Pro	Arg	Val	Asp	Phe	His	Trp	Lys	Phe	Val	Thr	His	Pro	Ile
											420		425		430
Ala	Ser	Asp	Asn	Phe	Tyr	Tyr	Pro	Gly	Tyr	Val	Gly	Ile	Gly	Thr	Gln
											435		440		445
Leu	Gln	Asp	Ser	Glu	Asn	Glu	Leu	Pro	Pro	Glu	Ala	Thr	Gly	Gln	Pro
											450		455		460
Asn	Tyr	Glu	Ser	Tyr	Ser	His	Arg	Leu	Ser	His	Ile	Gly	Leu	Ile	Ser
465											470		475		480
Ala	Ser	His	Val	Lys	Ala	Leu	Val	Tyr	Ser	Trp	Thr	His	Arg	Ser	Ala
											485		490		495
Asp	Arg	Thr	Asn	Thr	Ile	Glu	Pro	Asn	Ser	Ile	Thr	Gln	Ile	Pro	Leu
											500		505		510
Val	Lys	Ala	Phe	Asn	Leu	Ser	Ser	Gly	Ala	Ala	Val	Val	Arg	Gly	Pro
											515		520		525
Gly	Phe	Thr	Gly	Gly	Asp	Ile	Leu	Arg	Arg	Thr	Asn	Thr	Gly	Thr	Phe
											530		535		540
Gly	Asp	Ile	Arg	Val	Asn	Ile	Asn	Pro	Pro	Phe	Ala	Gln	Arg	Tyr	Arg
											545		550		560
Val	Arg	Ile	Arg	Tyr	Ala	Ser	Thr	Thr	Asp	Leu	Gln	Phe	His	Thr	Ser
											565		570		575
Ile	Asn	Gly	Lys	Ala	Ile	Asn	Gln	Gly	Asn	Phe	Ser	Ala	Thr	Met	Asn
											580		585		590
Arg	Gly	Glu	Asp	Leu	Asp	Tyr	Lys	Thr	Phe	Arg	Thr	Val	Gly	Phe	Thr
											595		600		605
Thr	Pro	Phe	Ser	Phe	Leu	Asp	Val	Gln	Ser	Thr	Phe	Thr	Ile	Gly	Ala
											610		615		620
Trp	Asn	Phe	Ser	Ser	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Ile	Glu	Phe
											625		630		640
Val	Pro	Val	Glu	Val	Thr	Tyr	Glu	Ala	Glu	Tyr	Asp	Phe	Glu	Lys	Ala
											645		650		655
Gln	Glu	Lys	Val	Thr	Ala	Leu	Phe	Thr	Ser	Thr	Asn	Pro	Arg	Gly	Leu
											660		665		670
Lys	Thr	Asp	Val	Lys	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu	Val
											675		680		685
Glu	Ser	Leu	Ser	Asp	Glu	Phe	Tyr	Leu	Asp	Glu	Lys	Arg	Glu	Leu	Phe
											690		695		700
Glu	Ile	Val	Lys	Tyr	Ala	Lys	Gln	Leu	His	Ile	Glu	Arg	Asn	Met	
											705		710		715

<210> 58
 <211> 719
 <212> PRT
 <213> Artificial sequence

<220>
 <223> PROTEIN cry1Ia5 Emb1. Accession No. Y08920

<400> 58
 Met Lys Leu Lys Asn Gln Asp Lys His Gln Ser Phe Ser Ser Asn Ala
 1 5 10 15
 Lys Val Asp Lys Ile Ser Thr Asp Ser Leu Lys Asn Glu Thr Asp Ile
 20 25 30
 Glu Leu Gln Asn Ile Asn His Glu Asp Cys Leu Lys Met Ser Glu Tyr

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Glu Asn Val Glu Pro Phe Val Ser Ala Ser Thr Ile Gln Thr Gly Ile
 35 40 45
 50 55 60
 Gly Ile Ala Gly Lys Ile Leu Gly Thr Leu Gly Val Pro Phe Ala Gly
 65 70 75 80
 Gln Val Ala Ser Leu Tyr Ser Phe Ile Leu Gly Glu Leu Trp Pro Lys
 85 90 95
 Gly Lys Asn Gln Trp Glu Ile Leu Phe Met Glu His Val Glu Glu Ile
 100 105 110
 Asn Gln Lys Ile Ser Thr Tyr Ala Arg Asn Lys Ala Leu Thr Asp Leu
 115 120 125
 Lys Gly Leu Gly Asp Ala Leu Ala Val Tyr His Asp Ser Leu Glu Ser
 130 135 140
 Trp Val Gly Asn Arg Asn Asn Thr Arg Ala Arg Ser Val Val Arg Ser
 145 150 155 160
 Gln Tyr Ile Ala Leu Glu Leu Met Phe Val Gln Lys Leu Pro Ser Phe
 165 170 175
 Ala Val Ser Gly Glu Glu Val Pro Leu Leu Pro Ile Tyr Ala Gln Ala
 180 185 190
 Ala Asn Leu His Leu Leu Leu Arg Asp Ala Ser Ile Phe Gly Lys
 195 200 205
 Glu Trp Gly Leu Ser Ser Glu Ile Ser Thr Phe Tyr Asn Arg Gln
 210 215 220
 Val Glu Arg Ala Gly Asp Tyr Ser Asp His Cys Val Lys Trp Tyr Ser
 225 230 235 240
 Thr Gly Leu Asn Asn Leu Arg Gly Thr Asn Ala Glu Ser Trp Val Arg
 245 250 255
 Tyr Asn Gln Phe Arg Arg Asp Met Thr Leu Met Val Leu Asp Leu Val
 260 265 270
 Ala Leu Phe Pro Ser Tyr Asp Thr Gln Met Tyr Pro Ile Lys Thr Thr
 275 280 285
 Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Ala Ile Gly Thr Val His
 290 295 300
 Pro His Pro Ser Phe Thr Ser Thr Thr Trp Tyr Asn Asn Asn Ala Pro
 305 310 315 320
 Ser Phe Ser Ala Ile Glu Ala Ala Val Val Arg Asn Pro His Leu Leu
 325 330 335
 Asp Phe Leu Glu Gln Val Thr Ile Tyr Ser Leu Leu Ser Arg Trp Ser
 340 345 350
 Asn Thr Gln Tyr Met Asn Met Trp Gly Gly His Lys Leu Glu Phe Arg
 355 360 365
 Thr Ile Gly Gly Thr Leu Asn Ile Ser Thr Gln Gly Ser Thr Asn Thr
 370 375 380
 Ser Ile Asn Pro Val Thr Leu Pro Phe Thr Ser Arg Asp Val Tyr Arg
 385 390 395 400
 Thr Glu Ser Leu Ala Gly Leu Asn Leu Phe Leu Thr Gln Pro Val Asn
 405 410 415
 Gly Val Pro Arg Val Asp Phe His Trp Lys Phe Val Thr His Pro Ile
 420 425 430
 Ala Ser Asp Asn Phe Tyr Tyr Pro Gly Tyr Ala Gly Ile Gly Thr Gln
 435 440 445
 Leu Gln Asp Ser Glu Asn Glu Leu Pro Pro Glu Ala Thr Gly Gln Pro
 450 455 460
 Asn Tyr Glu Ser Tyr Ser His Arg Leu Ser His Ile Gly Leu Ile Ser
 465 470 475 480
 Ala Ser His Val Lys Ala Leu Val Tyr Ser Trp Thr His Arg Ser Ala
 485 490 495
 Asp Arg Thr Asn Thr Ile Glu Pro Asn Ser Ile Thr Gln Ile Pro Leu
 500 505 510
 Val Lys Ala Phe Asn Leu Ser Ser Gly Ala Ala Val Val Arg Gly Pro
 515 520 525
 Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Asn Thr Gly Thr Phe
 530 535 540

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Gly Asp Ile Arg Val Asn Ile Asn Pro Pro Phe Ala Gln Arg Tyr Arg
 545 550 555 560
 Val Arg Ile Arg Tyr Ala Ser Thr Thr Asp Leu Gln Phe His Thr Ser
 565 570 575
 Ile Asn Gly Lys Ala Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Asn
 580 585 590
 Arg Gly Glu Asp Leu Asp Tyr Lys Thr Phe Arg Thr Val Gly Phe Thr
 595 600 605
 Thr Pro Phe Ser Phe Leu Asp Val Gln Ser Thr Phe Thr Ile Gly Ala
 610 615 620
 Trp Asn Phe Ser Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe
 625 630 635 640
 Val Pro Val Glu Val Thr Tyr Glu Ala Glu Tyr Asp Phe Glu Lys Ala
 645 650 655
 Gln Glu Lys Val Thr Ala Leu Phe Thr Ser Thr Asn Pro Arg Gly Leu
 660 665 670
 Lys Thr Asp Val Lys Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val
 675 680 685
 Glu Ser Leu Ser Asp Glu Phe Tyr Leu Asp Glu Lys Arg Glu Leu Phe
 690 695 700
 Glu Ile Val Lys Tyr Ala Asn Glu Leu His Ile Glu Arg Asn Met
 705 710 715

<210> 59

<211> 719

<212> PRT

<213> Artificial Sequence

<220>

<223> PROTEIN cry1Ib1 Emb1. Accession No. U07642

<400> 59

Met Lys Leu Lys Asn Pro Asp Lys His Gln Ser Leu Ser Ser Asn Ala
 1 5 10 15
 Lys Val Asp Lys Ile Ala Thr Asp Ser Leu Lys Asn Glu Thr Asp Ile
 20 25 30
 Glu Leu Lys Asn Met Asn Asn Glu Asp Tyr Leu Arg Met Ser Glu His
 35 40 45
 Glu Ser Ile Asp Pro Phe Val Ser Ala Ser Thr Ile Gln Thr Gly Ile
 50 55 60
 Gly Ile Ala Gly Lys Ile Leu Gly Thr Leu Gly Val Pro Phe Ala Gly
 65 70 75 80
 Gln Ile Ala Ser Leu Tyr Ser Phe Ile Leu Gly Glu Leu Trp Pro Lys
 85 90 95
 Gly Lys Ser Gln Trp Glu Ile Phe Met Glu His Val Glu Glu Ile Ile
 100 105 110
 Asn Gln Lys Ile Leu Thr Tyr Ala Arg Asn Lys Ala Leu Ser Asp Leu
 115 120 125
 Arg Gly Leu Gly Asp Ala Leu Ala Val Tyr His Glu Ser Leu Glu Ser
 130 135 140
 Trp Val Glu Asn Arg Asn Asn Thr Arg Ala Arg Ser Val Val Lys Asn
 145 150 155 160
 Gln Tyr Ile Ala Leu Glu Leu Met Phe Val Gln Lys Leu Pro Ser Phe
 165 170 175
 Ala Val Ser Gly Glu Glu Val Pro Leu Leu Pro Ile Tyr Ala Gln Ala
 180 185 190
 Ala Asn Leu His Leu Leu Leu Arg Asp Ala Ser Ile Phe Gly Lys
 195 200 205
 Glu Trp Gly Leu Ser Ala Ser Glu Ile Ser Thr Phe Tyr Asn Arg Gln
 210 215 220
 Val Glu Arg Thr Arg Asp Tyr Ser Asp His Cys Ile Lys Trp Tyr Asn
 225 230 235 240

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Thr Gly Leu Asn Asn Leu Arg Gly Thr Asn Ala Lys Ser Trp Val Arg
 245 250 255
 Tyr Asn Gln Phe Arg Lys Asp Met Thr Leu Met Val Leu Asp Leu Val
 260 265 270
 Ala Leu Phe Pro Ser Tyr Asp Thr Leu Val Tyr Pro Ile Lys Thr Thr
 275 280 285
 Ser Gln Leu Thr Arg Glu Val Tyr Thr Asp Ala Ile Gly Thr Val His
 290 295 300
 Pro Asn Gln Ala Phe Ala Ser Thr Thr Trp Tyr Asn Asn Asn Ala Pro
 305 310 315 320
 Ser Phe Ser Ala Ile Glu Ala Ala Val Ile Arg Ser Pro His Leu Leu
 325 330 335
 Asp Phe Leu Glu Lys Val Thr Ile Tyr Ser Leu Leu Ser Arg Trp Ser
 340 345 350
 Asn Thr Gln Tyr Met Asn Met Trp Gly Gly His Arg Leu Glu Ser Arg
 355 360 365
 Pro Ile Gly Gly Ala Leu Asn Thr Ser Thr Gln Gly Ser Thr Asn Thr
 370 375 380
 Ser Ile Asn Pro Val Thr Leu Gln Phe Thr Ser Arg Asp Val Tyr Arg
 385 390 395 400
 Thr Glu Ser Leu Ala Gly Leu Asn Leu Phe Leu Thr Gln Pro Val Asn
 405 410 415
 Gly Val Pro Arg Val Asp Phe His Trp Lys Phe Pro Thr Leu Pro Ile
 420 425 430
 Ala Ser Asp Asn Phe Tyr Tyr Leu Gly Tyr Ala Gly Val Gly Thr Gln
 435 440 445
 Leu Gln Asp Ser Glu Asn Glu Leu Pro Pro Glu Thr Thr Gly Gln Pro
 450 455 460
 Asn Tyr Glu Ser Tyr Ser His Arg Leu Ser His Ile Gly Leu Ile Ser
 465 470 475 480
 Ala Ser His Val Lys Ala Leu Val Tyr Ser Trp Thr His Arg Ser Ala
 485 490 495
 Asp Arg Thr Asn Thr Ile Glu Pro Asn Ser Ile Thr Gln Ile Pro Leu
 500 505 510
 Val Lys Ala Phe Asn Leu Ser Ser Gly Ala Ala Val Val Arg Gly Pro
 515 520 525
 Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Asn Thr Gly Thr Phe
 530 535 540
 Gly Asp Ile Arg Val Asn Ile Asn Pro Pro Phe Ala Gln Arg Tyr Arg
 545 550 555 560
 Val Arg Ile Arg Tyr Ala Ser Thr Thr Asp Leu Gln Phe His Thr Ser
 565 570 575
 Ile Asn Gly Lys Ala Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Asn
 580 585 590
 Arg Gly Glu Asp Leu Asp Tyr Lys Thr Phe Arg Thr Ile Gly Phe Thr
 595 600 605
 Thr Pro Phe Ser Phe Ser Asp Val Gln Ser Thr Phe Thr Ile Gly Ala
 610 615 620
 Trp Asn Phe Ser Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe
 625 630 635 640
 Val Pro Val Glu Val Thr Tyr Glu Ala Glu Tyr Asp Phe Glu Lys Ala
 645 650 655
 Gln Glu Lys Val Thr Ala Leu Phe Thr Ser Thr Asn Pro Arg Gly Leu
 660 665 670
 Lys Thr Asp Val Lys Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val
 675 680 685
 Glu Ser Leu Ser Asp Glu Phe Tyr Leu Asp Glu Lys Arg Glu Leu Phe
 690 695 700
 Glu Ile Val Lys Tyr Ala Lys Gln Ile His Ile Glu Arg Asn Met
 705 710 715

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<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> PROTEIN

<221> VARIANT

<222> 1, 2, 3, 5, 6, 7, 8, 9, 10, 12, 13, 14, 15, 16, 19, 20, 21,
22, 24, 25, 26, 27, 28, 29, 30, 31, 33
<223> Xaa = Any Amino Acid

<400> 60

Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa
1 5 10 15
Cys Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys
20 25 30
Xaa

<210> 61

<211> 439
<212> DNA
<213> Paecilomyces sp.

<400> 61

tctacttctt catctcacgc catatatcct cccaaaatca cacctttcc ttcaccatgc 60
aaatctccgc cgtcattgtc gcactcttcg ccagcgccgc catggccggc aagatctgca 120
ctccctgtcgg agttgtacgt attttcatcc atttccyca ccactccctt aacatgaagc 180
aactttctt tctcttaga aatgtcccgcc ggctcttcct tgctgccccg gacttcgtg 240
catcggccgc gtcaacgtaa gtcaccatgg atctggcaag cgagaccata acatgacgca 300
gtataactaac cctggccgtt atagaacaag gttgtgagtc gacatgttkt acaacctta 360
caaacgcgcg cactaatgac aacggtagtg ccggtaattc tagtgtcgca acttttgagc 420
gtgggataag tatgcttcg 439

<210> 62

<211> 438
<212> DNA
<213> Paecilomyces sp.

<400> 62

attacccaag tttgagggca ttcaatttca cacagtctca cgctttcgac gcatctactt 60
cttcgttca cgccatatat cctcccaaaa tcacacctct tccttccacca tgcaaatctc 120
cgccgtcatt gtgcactct tcgcccagcgc cgccatggcc ggcagatct gcactccgtc 180
tggagttaaa tggcccgccg ctcttccttg ctgccccgga ctcgcgtgca tcggccgggt 240
caacaacaag gttgcccgtt aattctagtg tcgcaacttt tgagcgtggg ataagtatgc 300
ttcgttctgtt gtatggagtt ctccctccgga gtttaagctc gggccggtcgaa cagcgggtct 360
gctatacttg atttacagc gatactatttg atagaatgc acatcttcat tcatgcgtca 420
tgaaaaaaaaaaaaaaa 438

<210> 63

<211> 6
<212> PRT
<213> Artificial Sequence

<220>

<223> INSECTICIDAL PROTEIN MOTIF

<400> 63

Leu Pro Cys Cys Pro Gly
1 5

SYN-128.ST25.txt

<210> 64
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> INSECTICIDAL PROTEIN MOTIF

<400> 64
Ile Cys Thr Pro Ala
1 5

<210> 65
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> PROTEIN REGION N-TERMINAL

<221> VARIANT
<222> 1, 2
<223> Xaa = Any Amino Acid

<400> 65
Xaa Xaa Ile Cys Thr
1 5